

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: January 4, 2005, 12:11:19 ; Search time 41 Seconds
(without alignments)
624.236 Million cell updates/sec

Title: US-10-006-867-2
Perfect score: 1392
Sequence: 1 MWNFQQGLSFLPSALVIWTS.....YDTAPCPINNERTRLLSRDI 266

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	361.5	26.0	246	2 T13747	hypothetical prote
2	288	20.7	271	2 T19654	hypothetical prote
3	120	8.6	547	2 C88456	protein W03A5.2 [i
4	103	7.4	332	2 E69312	nitrate reductase
5	98.5	7.1	1120	2 AI0561	integral membrane
6	97	7.0	604	2 E72523	carbon starvation
7	96	6.9	495	2 S43882	NADH2 dehydrogenas
8	94	6.8	495	1 S16447	NADH2 dehydrogenas
9	93.5	6.7	379	2 D96506	hypothetical prote
10	93.5	6.7	429	2 F71651	putrescine-ornithi
11	93	6.7	1120	2 F90693	mechanosensitive c
12	93	6.7	1120	2 B85544	mechanosensitive c
13	93	6.7	1120	2 H64776	probable membrane
14	92.5	6.6	473	2 AE0801	probable amino aci
15	91.5	6.6	373	2 T24487	hypothetical prote
16	91.5	6.6	712	2 T02479	potassium transpor
17	90.5	6.5	614	2 E86194	hypothetical prote
18	90	6.5	400	2 C82503	hypothetical prote
19	90	6.5	492	2 S59107	NADH2 dehydrogenas
20	90	6.5	528	2 S19366	hypothetical prote
21	89.5	6.4	440	2 B64090	dicarboxylate tran
22	89.5	6.4	443	2 AE1706	hypothetical prote
23	89.5	6.4	495	2 G71019	hypothetical prote
24	89.5	6.4	599	2 T24333	hypothetical prote
25	89	6.4	428	2 AI0034	probable transmemb
26	89	6.4	757	2 T42693	hypothetical prote
27	88.5	6.4	430	2 E75217	transporter PAB217
28	88.5	6.4	844	2 T23656	hypothetical prote
29	88	6.3	1165	2 A46180	adenylyl cyclase t

30	87.5	6.3	233	2 E70114	hemolysin III (ypl
31	87.5	6.3	429	2 D82181	GGDEF family prote
32	87.5	6.3	482	2 B69803	metabolite transpo
33	87.5	6.3	540	2 T24675	hypothetical prote
34	87	6.2	396	2 B91013	bicyclomycin resis
35	87	6.2	396	2 D85857	bicyclomycin resis
36	87	6.2	435	2 C95975	probable polysacch
37	87	6.2	613	2 C83496	glutathione-regula
38	86.5	6.2	400	2 C69757	transporter homolo
39	86.5	6.2	583	2 AH1151	glycerophosphoryl
40	86.5	6.2	770	2 G72589	hypothetical prote
41	86	6.2	373	2 D89865	hypothetical prote
42	86	6.2	389	2 G75133	hypothetical prote
43	86	6.2	396	1 E64987	bicyclomycin resis
44	86	6.2	703	2 E86146	F22L4.12 protein -
45	85.5	6.1	295	2 E81179	spermidine/putresc

ALIGNMENTS

RESULT 1

T13747

hypothetical protein 22E5.9 - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C:Accession: T13747

R:Murphy, L.; Harris, D.; Barrell, B.

submitted to the EMBL Data Library, April 1999

A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.

A:Reference number: Z17668

A:Accession: T13747

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-246 <MUR>

A:Cross-references: UNIPROT:O77262; EMBL:AL031765; NID:e1371523; PID:e1326055; PIDN:CAA

C:Genetics:

A:Cross-references: FlyBase:FBgn0000667

A:Introns: 22/2; 63/1; 192/2

A>Note: EG:22E5.9

C:Superfamily: Caenorhabditis elegans hypothetical protein C33A11.2

Query Match	26.0%	Score	361.5;	DB 2;	Length	246;
Best Local Similarity	33.6%	Pred.	No. 3.5e-24;			
Matches	78;	Conservative	50;	Mismatches	91;	Indels 13; Gaps 4;
Qy	11	LPSALVIWTSAA	FIPSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIAT	70		
Db	7	LPVLTFLIFQV	TLGTIYFAVLEGHVPTVPYISDAATYSPESCVFGLINIGSVLLGIT	66		
Qy	71	IYRYKQVHAL--	--SPE-ENVIKLNKAGLVGLSLCLGLSIVANFQKTLTFAAHVSGAV	126		
Db	67	IYRYRQVLQLY	EHHPDLGSLVRQNRLLALWFLVSLGLSIFVGNFQETNVRIVHFIGAF	126		
Qy	127	LTFGMGSLYMF	VQTIILSYQMOPKIHGKQVFWIRLLLVWCGVSALSML---TCSSVLHSG	183		
Db	127	CCFCGCTLYF	WMQALISYLIFPMSGTRINAHRLGMSVVCTILFILLAVTGMVSHILPKG	186		
Qy	184	NFGTDLEQKL	HNWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISL	235		
Db	187	-----QNP	RKWYPSDGGWYFHWSSISEWVIATVFSFFILSFTNEFRDVS	232		

RESULT 2

T19654

hypothetical protein C33A11.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T19654

R:Gajadaty, S.

submitted to the EMBL Data Library, August 1996

A:Reference number: Z19158

A:Accession: T19654

C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24487
R;Lloyd, C.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z19897
A;Accession: T24487
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-373 <WIL>
A;Cross-references: UNIPROT:Q22188; EMBL:Z68219; PIDN:CAA92481.1; GSPDB:GN00022; CESP:T05A1
A;Experimental source: clone T05A1
C;Genetics:
A;Gene: CESP:T05A1.1
A;Map position: 4
A;Introns: 48/2; 106/3; 219/2; 254/1; 280/1; 309/1; 327/2

Query Match	6.6%;	Score 91.5;	DB 2;	Length 373;
Best Local Similarity	23.0%;	Pred. No. 2;		
Matches	50;	Conservative 34;	Mismatches 82;	Indels 51; Gaps 11;

QY	69	ATIIVRYKQVHALSPBENVIIKLNKAGLVGLISCLGLSIVANFQKTTLFAAH-----	121
Db	46	AVLYLTMKH-RQLQTVQNFIILNLCASNVLMLCLTSLPITFITNVYKQWFFSSPVCKLPL	104
QY	122	VSQA---VLTFGMGLYMFVQTIILSYQMOPKIHGKQVFIWIRLLVIWCGVSALSMLTCS	178
Db	105	VQGSIFVSTFSLSAIALDRYNLVVRPHKQKLSSRSAMMIAL--IW----VISVVVCM	158
QY	179	VLHSGNFGTDLE-QKL-----HWNPED--KGYVLHMITTAAEWSMSFSFFGFFLT	225
Db	159	-----YGWYMDVEKLNGLCGEYCEHWPPLAEVRKGYTFLVLIT----QLFFPEATMAFC	208
QY	226	YIRDFQKISLRVEANLHGLTLYDTAPCPINNERTRL	262
Db	209	YNYIFSRLRQRVETKLKKL-----SERSOLL	234

Search completed: January 4, 2005, 12:20:57
Job time : 43 secs